

RhUS28.1

10	20	30	40	50	60
ATGAATAACA	CATCTTGCAA	CTTCAACGTC	ACTCTCAACG	CATCGGCACC	AAGCCGATAC
70	80	90	100	110	120
ATAGCTATTG	CTATGTACAG	CATTGTTATC	TGTATCGGGT	TGGTTGGAAA	CCTGCTGTTA
130	140	150	160	170	180
TGCATCGTGT	TAGTCAAGAA	ACGCAAACTG	CGATATTCCA	GCGATGTTTA	TTTMTCCAC
190	200	210	220	230	240
GCCTCTATGG	CCGACCTCGT	CAGCACTGTC	ATGCTACCGC	TCTGGCTACA	TTATGTCCTC
250	260	270	280	290	300
AACTTTGCCC	AACTCTCTCG	AGGAGCCTGT	ATCAGCTTTT	CGGTGACTTT	CTATGTTCCC
310	320	330	340	350	360
CTTTTCGTTT	AGGCCTGGTT	ACTCATTTCC	ATCGCTATGG	AGCGATATTC	CAACTTAGTA
370	380	390	400	410	420
TGGATGGCAC	CCATTAGCGT	TAAGACGGCC	TTTAAACACT	GCATAGGAAC	CTGGATCGTA
430	440	450	460	470	480
TCTGCCTTCG	TGGCATCACC	CTACTACGCA	TACAGAAACT	CACACGACGA	ACACGAATGC
490	500	510	520	530	540
ATTCTAGGAA	ACTACACTTG	GCACATTAAC	GAACCGCTAC	ACACGTGTAT	GGATGTGGTG
550	560	570	580	590	600
ATCATAGTAT	GGACCTTTTT	GGCCCCAGTA	CTGGTAACCA	TTATAGCAAG	CGTCAAAATG
610	620	630	640	650	660
AGACGAACGA	CCTGGGGCAA	TACTAGGTTA	AACGAAAAGA	ACAGCGACAT	TCTTATAGTA
670	680	690	700	710	720
CTAGTTGTCA	TGACAGTGTT	CTTTTGGGGA	CCGTTTAATA	TCGTGTGGT	TATTGACAAT
730	740	750	760	770	780
ATTTTACAGA	GATACTATGA	TACCACGAAT	TGCGATGTAG	AAAAGATTAA	ACATATCATG
790	800	810	820	830	840
GCTATGATCT	CAGAAGCCAT	TGTTTATTTT	CGCGGTATTA	CAGCACCTAT	TATTTATGTA
850	860	870	880	890	900
GGGATTAGTG	GCAGATTTCG	CGAAGAGATT	TACTCTCTGT	TTAGACGCCA	GCCGTATAAC
910	920	930	940	950	960
GATTTGGACC	COGATGCCAA	TCAATTCATG	ATTGAACTCA	CTAGCCAGGG	AAGAAGTAGA
970	980	990	1000	1010	1020
AATAGAAATG	CTAGACAATC	GGAAAGCAAT	GTACCGCAAC	CAGAAGAATG	CTTCTGGTAA
1030	1040	1050	1060	1070	1080
.....

FIG. 1

RhUS28.2

10	20	30	40	50	60
ATGACCAACG	CCGGACACTG	TCACATAAAC	GAAAGTCTCG	CGTCGTATGG	AATCGCTCCC
70	80	90	100	110	120
GCAGCTACCA	TTACCTTATA	CAGCATTGCG	GGAATCTGCG	GTGTCACGGG	AAATCTGTTA
130	140	150	160	170	180
ATACTTTTGG	TTTGTTCAC	GAGACGCATA	CACTGGTTTCG	CAAATGACAT	CTACTATCTC
190	200	210	220	230	240
AACATGATCT	TTACAGACTT	TCTTGTTTTT	ATTACATTAC	CCGCCTGGGT	TTACTACCTG
250	260	270	280	290	300
CTGAATTACA	CACAACTCTC	ACACTATGCC	TGCATTGCTC	TATCATTGT	TTTTTACGTT
310	320	330	340	350	360
TCCATTTTTA	TTCAAGCTGA	CTTTATGGTA	GCAGTGGCTA	TCGAGCGTTA	TCGAAGCCTA
370	380	390	400	410	420
GTGAAAAACA	AACCCCTTAG	CGTAAAAAAA	GCCAGCGTCA	GCTGCGCGTG	CATCTGGATC
430	440	450	460	470	480
ATTGTTATTA	TAGTGTCTTC	ACCATACTAC	ATGTTTAGAT	CGCAACACGA	AACAAATTCT
490	500	510	520	530	540
TGCATTCTAG	GAAACTACAC	CTGGCATATG	AACAGTCCTT	TTCGCACCAC	AATGGACGCA
550	560	570	580	590	600
TCCATTAACA	TTTGGTCTTT	TGTCGTTCCG	GCCGTGACGA	CCTTGTTAAT	AGCCAGACGA
610	620	630	640	650	660
ATTTATGTAT	GTACTTCAGG	CAACAAAAAA	ATGAACGCCA	GAGCCAGTGG	TTTGTTAGAG
670	680	690	700	710	720
GCCATGGTGA	TTAGCATGTT	ATTCTTCGGA	GGACTTTTCA	ACCTGAACAT	CTTTCGAGAC
730	740	750	760	770	780
ATAGTTTCGG	ACACATCGGA	AGACAATAAA	GA CTGCACAT	ATCTTAAGCA	GGAACACTTT
790	800	810	820	830	840
ATTTCGCATGG	TCGGTGTGGC	CCTCGTTTAC	GGGCGCGCTA	TATTCAACCC	TTTTATGTAT
850	860	870	880	890	900
ATGTGTGTGA	GTACCAGATT	CGGCCAAGAA	ATAAAATGTT	TGTTTATGCG	AATACCTTAT
910	920	930	940	950	960
GAAACACTAG	ATGCAGAACA	CGCTAAACTC	ATGGTTAATT	TAAAAACAG	AAATGCTAAT
970	980	990	1000	1010	1020
GTACCCGATC	CTAAACCTCG	TGAATATGAA	TCTGTGTTAT	AG.....

FIG. 2

RhUS28.3

10	20	30	40	50	60
ATGACCAACA	CTAACAATAC	GACTTGTCAT	CTCAACGGAA	CTTTCGAAAC	TTTTAAAATC
70	80	90	100	110	120
ACCCGTCCAG	TAGCCATCAG	CGCCTACACT	GTACTCGTGG	TTATCGGACT	TTTGGGAAAC
130	140	150	160	170	180
ATTGTGCTGC	TCAGCGTGCT	CGTCGTGAAA	CGCAAGCTCA	AGTTTCCGAA	TGACATTTAC
190	200	210	220	230	240
TTTTTCAACG	CGTCTTTGGC	AGACGTTTTT	GCCGTCTGCA	TGTTGCCCGC	CTGGGTAAAC
250	260	270	280	290	300
TATGCACTGG	ACTCCACACA	ACTTAGCAAG	TTCTCATGTA	TCACTTTTAC	GTTTGGTTTT
310	320	330	340	350	360
TACGTCTCCC	TGTTTCATCCA	GGCCTGGATG	CTCATTCTGG	TCACCCTGGA	GCGATACGGA
370	380	390	400	410	420
TCTCTAGTCT	GGATCGCCCC	GATCACCAGA	AACAAAGCCA	TAGCGAATTG	TGTACTCTTT
430	440	450	460	470	480
TGGCTTGTTT	CCATCTTCTT	GGCCGCACCT	TACTACTCTT	TTAGAAACGA	AAGCAACGAA
490	500	510	520	530	540
CACCAATGCA	TCATGAGAAA	CTATACCTGG	AGCGTTGGTG	AAACATGGCA	CATAGCCCTG
550	560	570	580	590	600
GATTTCTTAA	TTACGCTCAT	TACATTTATC	ATGCCAGTGA	CTATTGTGTT	AGCTCTGAGT
610	620	630	640	650	660
TTCAAAATGG	CCAGATGGTC	AACCTTTGGT	TACAGAAAACC	TCACCAGCAG	AACCAGTCTT
670	680	690	700	710	720
ATCCTTATTT	TGATACTGAC	AGTAGCAGCA	GGGTTCTGGG	GACCTTTTCA	CCTATTTATG
730	740	750	760	770	780
TTTATAGAAA	ACGTGGCAGG	GCAGATTTAC	CACATTCAAA	AGGATTGCTG	GTACTTACAG
790	800	810	820	830	840
CTCAGACACT	TGTGTAGCTT	GATGACCGAA	ACCCTAGTGT	TTCTACGTTT	AGTTTTTAAC
850	860	870	880	890	900
CCTTATATTT	ATATGATAAT	CAGTTACAAG	TTTAGGCAGC	AGGTGCGCAG	TCTACTCAAG
910	920	930	940	950	960
CGTACTCAGT	ATGATGCTTT	GGACACGACT	CAGTTAGCAG	AAACTATGCA	GCTGAAAGCG
970	980	990	1000	1010	1020
AAAGGTGTGC	CGGTGTCCGA	CCCCGCGCCG	CATGACTGCG	AATGCTTTTT	GTAA.....

FIG. 3

RhUS28.4

10	20	30	40	50	60
GAATTCGAGC	CAGCACAACA	TAAGCGTGTT	TCTCTCCATT	GGAGCAGGGC	CCGTCATTAC
70	80	90	100	110	120
CGGATACACG	TGCGTTTTTC	TGTTCCGGGAT	TCTGGGACAC	TTTACTTGT	ATTGGAAAAA
130	140	150	160	170	180
CCATCAGAGA	CGACACCGGA	CAAACAGTTT	CAGTGATGTT	TTATTTGAC	ATCTCATGAT
190	200	210	220	230	240
CACCGAAGAG	GTCTTTACCC	TCACCATTCC	CGTCTGGGCG	TATCACTTAA	CTACTCACGG
250	260	270	280	290	300
CAACTTACCG	GGCTCGTGGT	GCCGAAGTCT	CACCTTCGTT	TTTTATCTAA	CGGTATTTCG
310	320	330	340	350	360
TCGTGCCTTC	TTTACCTGC	TCCTCATCTG	GGACCGATAC	AGCGTAATCA	TCTGCAGACA
370	380	390	400	410	420
CCCTCTCCCC	GTAAATCTGA	ACTACAGTCA	GGTCATAGGC	CTGTCTGTCT	GGCTGGTTGC
430	440	450	460	470	480
CGTACTGTCA	GCATCACCGT	TCTCCATTTT	TAACGGAAGT	GTGAAACAAT	GCCTGGGCAA
490	500	510	520	530	540
CATGGGCAGC	ATACCCAGCG	AATCGTCTGC	CGTTCTTAAC	CTGGAAGTGC	ACCTGTGCTC
550	560	570	580	590	600
CTTCTGGTTA	CCGCTCATCA	TGTCGGCTAA	CTGTTACTAC	CAAGCAAAAC	GCCGAGCATC
610	620	630	640	650	660
GCCTGACCAA	CTCCACGAAC	TTTACCGATG	CAGTTTGCTA	ATTACCATTA	TCACAACTTA
670	680	690	700	710	720
CGCTATCGTA	TGGTTTCCTT	TCCATCTCGC	TTTACTCATA	GACGCCCTGA	TTAGCATAAG
730	740	750	760	770	780
CCATGTAGAA	CCCTCTAGCG	CTCTCCACTG	GGCATCCATT	GTCGTTACCT	GTAAATCATT
790	800	810	820	830	840
TACATTTGTA	TATGCGGGCA	TAAGCCCACT	AGTGTATTTT	ACATGCTGCC	CCACCGTACG
850	860	870	880	890	900
TCGCGAACTG	CTGATGTCTC	TACGTCCATT	CTTCACCTGG	ATTTCAGCA	AAACGCGGCG
910	920	930	940	950	960
AGGCTACGCT	CCGATTAAAA	CACAACCTTT	AAACATCCCC	GACGAGCCGA	TAGATAACAA
970	980	990	1000	1010	1020
GTCACCGCAC	CTGTAAACG	AATAA.....

FIG. 4

RhUS28.5

10	20	30	40	50	60
ATGACTACCA	CCACAATGAG	TGCTACCACG	AATTCAGTA	CCACGCCTCA	AGCAAGCAGC
70	80	90	100	110	120
ACCACGATGA	CAACGAAGAC	AAGCACTCCT	GGCAATACAA	CTACTGGCAC	TACGTCCACC
130	140	150	160	170	180
CTGACAACGA	TATCAACAAC	TTCTAATGCT	ACCAGCATAA	CGTCTAATTT	AAGCACTACC
190	200	210	220	230	240
GGAAACCAA	CTGCAACTAC	CAATGCTACT	ACCTTCAGTT	CCACATTAAC	AACATCTACA
250	260	270	280	290	300
AATATAAGCA	GTACATTTTC	GACAGTTTCT	ACCGTCGCAT	CCAATGCAAC	ATGTAATTCT
310	320	330	340	350	360
ACAATCACAA	CGAATATTAC	AACTGCTTTT	ACTACAGCAG	CAAACACTAC	CGCAAGCAGC
370	380	390	400	410	420
CTCACCAGCA	TCGTAAC TTC	ACTTGCCACT	ACCATGAAA	CCACATCATT	TGATTATGAT
430	440	450	460	470	480
GAGTCAGCAG	AAGCTTGCAA	CTTAACAGAC	ATCGTTCATA	CTACTAGATC	AGTGACAGTT
490	500	510	520	530	540
ACTTTCTATA	CTATCATATT	CATACTCGGC	CTTTTGGGAA	ACTTTCTGGT	TCTTATGACC
550	560	570	580	590	600
ATCATTTGGA	ACCGTCGCAT	TTCCTTTATG	GTTGAAATAT	ATTTTCGTTAA	TCTAGCAATC
610	620	630	640	650	660
TCCGATCTTA	TGTTTGATG	TACTTTACCA	TTTTGGATAA	TGTATCTTCT	TGAGCACGAC
670	680	690	700	710	720
GTCATGTCAC	ATGCATCCTG	TGTAGCAATG	ACAGCCATTT	TTTATTGCGC	GCTGTTTGCC
730	740	750	760	770	780
AGCACTGTTT	TCCTCTTGCT	AATTGTTTTA	GACAGATGTT	ACGCTATTCT	ATTAGGTACA
790	800	810	820	830	840
GAAAAAGCAA	ATAGACGTTT	ATTGCGCAAT	GCTGTTTCTG	GATGCATGCT	CATGTGGGGA
850	860	870	880	890	900
TTGTGTTTCA	TTTTAGCATT	ACCTCATTTT	ATCTTTATGA	AGAAAGGAAC	CAACGTATGT
910	920	930	940	950	960
GTAGCAGAGT	ATGAACCAGG	ACTTAACAAT	TTCTATGTTA	TTTTTATCAA	TACTGAGGTG
970	980	990	1000	1010	1020
AACCTATGCA	CCCTAGTTTT	GCCAGCCGCA	GCCATTATCT	ACTGGTATCT	TAAACTAACC
1030	1040	1050	1060	1070	1080
AAAGCACTCA	AAACCCATGA	ACGACTGCGT	CATAGGCTAA	CGTCTCTAAA	CATAGTGTTA
1090	1100	1110	1120	1130	1140
GCTGTGTGCA	TGTATTGTC	TTTGTTTTGG	CTGCCGTATA	ATCTCATGCT	TATGATGTAT
1150	1160	1170	1180	1190	1200
AGCTTAGTTC	ACATGCAGAT	ACCTTGGGAA	TGCAGCTCTG	AAAAAATACT	GAGACGAAGT
1210	1220	1230	1240	1250	1260
TTAATTATTA	CAGAATCCAT	CGCCCTCAGT	CACTGTTGCA	TCAACCCCAT	TATCTACTTG

FIG. 5A

RhUS28.5

1270	1280	1290	1300	1310	1320
CTCTTCGGAC	CTCGCTGTCG	AAGCGAGTTC	TGTCACCTGT	TGCGATGTTG	CTTTACGCGC
1330	1340	1350	1360	1370	1380
TTATGTCCAC	ACAGATCCTG	GAGTTCATA	CGTGCAGAGA	CGGTGTCCAT	CAGTCTCAGT
1390	1400	1410	1420	1430	1440
CACTCACAGG	TATCTGCATC	ATCTGAGGAT	GATGACAACG	ATGTGCATGA	TGAATTGCAA
1450	1460	1470	1480	1490	1500
TTTTTAATTT	GA.....

FIG. 5B

RhUL33

10	20	30	40	50	60
ATGACCAATC	TTTACTCTGC	CAATTTTCTC	ACCTTGATAG	TACTTCCTTT	TATCGTTTTA
70	80	90	100	110	120
AGCAATCAAC	ACCTTTTACC	TGCCAGTGCA	GTAACCTGTA	AATTTCTCTC	CCTGTTGTAC
130	140	150	160	170	180
TACTCTAGCT	GCAGCGTAGG	TTTTGCTACA	GTGGCACTGA	TAGCGGCCGA	CCGATACCGA
190	200	210	220	230	240
GTGATTCATC	GCCGAACTCA	AGCTCGCCAA	TCCTACCGTA	ACACATATAT	GATAGTAGGC
250	260	270	280	290	300
TTAACGTGGC	TCATTGGCTT	GATCTGCGCT	ACCCCCGGGG	GGGTCTACAC	AACCATTGTA
310	320	330	340	350	360
GCTCACCGCG	ATGGGGAAAG	TGATGCTCAA	AGACACAATA	CTTGCAATTAT	GCACTTTGCG
370	380	390	400	410	420
TATGATGAAG	TTTACGTCCT	CATGGTCTGG	AAACTTCTCA	TCGTTTTAGT	CTGGGGCATA
430	440	450	460	470	480
GTGCCAGTTG	TCATGATGAG	CTGGTTTTAC	GCGTTTTTTT	ACAATACTGT	ACAAAGAACA
490	500	510	520	530	540
GCCAAAAAAC	AACAACGTAC	GTTGAAATTC	GTAAAGGTAT	TACTCCTGTC	ATTCATCATC
550	560	570	580	590	600
ATCCAAACTC	CCTATGTGTC	AATCATGATT	TTTAACACGT	ATGCCACCGT	AGGATGGCCG
610	620	630	640	650	660
ATGGAATGCG	CCGATCTAAC	TAGACGCCGA	GTCATCAACA	CGTTTTCCCG	TCTCGTCCCC
670	680	690	700	710	720
AATCTACATT	GCATGGTCAA	CCCCATCCTC	TACGCTCTCA	TGGGAAATGA	CTTTGTGTCT
730	740	750	760	770	780
AAAGTGGGCC	AATGCTTTTCG	GGGGGAATC	ACGAACCGTC	GAACTTTTCT	GCGTTCCAAG
790	800	810	820	830	840
CAACAAGCCC	GCAACTCGGA	CGATGTACCG	ACAATTGTCA	GTCAACAACC	CGCCACACCC
850	860	870	880	890	900
ACCATCGTCA	ATAAGCCCGA	AAAAAACCCG	CACGTAAAC	GCGGTGTATC	TTTCAGCGTC
910	920	930	940	950	960
AGCGCATCTT	CCGAACTCGC	AGCGGCCAAA	AAAGCCAAAG	ACAAAGCCAA	GCGGCTTTCC
970	980	990	1000	1010	1020
ATGTCCCACC	AAAACCTACG	TCTGACGTGA

FIG. 6

RhUL33 spliced

10	20	30	40	50	60
ATGGCAGTCA	CTTTACGAGG	CGGCAGCCCG	ATAAACTTTA	AACTCATGAT	TGTCAGCCAC
70	80	90	100	110	120
AGAAACCGGA	AATTTACGGA	GATACGGCTG	TTTCAGCGTT	CTGCTATCCG	TCCAGGCGGG
130	140	150	160	170	180
TTATGGAAAC	CATTCTTCAC	AACCGAACG-	-----	-----	-----
190	200	210	220	230	240
-----	-----	-----	-----	-----AGTGA	AACTAATTCC
250	260	270	280	290	300
ATTTTGCACA	TCAACACCAC	CTGCAATGTG	ACCGACTCAC	TGTACGCCGC	CAAAC TAGGC
310	320	330	340	350	360
GAAGCCCTCG	TGAACAGCGC	GCTAGCTTTA	TTCCGTACCC	CCCTCAACGC	CATCGTCTCT
370	380	390	400	410	420
GTCACACAGC	TATTGGCCAA	CCGAGTTCAT	GGATACTCCA	CCCCGATTAT	CTACATGACC
430	440	450	460	470	480
AATCTTTACT	CTGCCAATTT	TCTCACCTTG	ATAGTACTTC	CTTTTATCGT	TTTAAGCAAT
490	500	510	520	530	540
CAACACCTTT	TACCTGCCAG	TGCAGTAACC	TGTAAATTTT	TCTCCCTGTT	GTACTACTCT
550	560	570	580	590	600
AGCTGCAGCG	TAGGTTTTCG	TACAGTGGCA	CTGATAGCGG	CCGACCGATA	CCGAGTGATT
610	620	630	640	650	660
CATCGCCGAA	CTCAAGCTCG	CCAATCCTAC	CGTAACACAT	ATATGATAGT	AGGCTTAACG
670	680	690	700	710	720
TGGCTCATTG	GCTTGATCTG	CGCTACCCCC	GGGGGGGTCT	ACACAACCAT	TGTAGCTCAC
730	740	750	760	770	780
CGCGATGGGG	AAAGTGATGC	TCAAAGACAC	AATACTTGCA	TTATGCACTT	TGCGTATGAT
790	800	810	820	830	840
GAAGTTTACG	TCCTCATGGT	CTGGAAACTT	CTCATCGTTT	TAGTCTGGGG	CATAGTGCCA
850	860	870	880	890	900
GTTGTCAATG	TGAGCTGGTT	TTACGCGTTT	TTTTACAATA	CTGTACAAAG	AACAGCCAAA
910	920	930	940	950	960
AAACAACAAC	GTACGTTGAA	ATTCGTAAAG	GTATTACTCC	TGTCATTTCAT	CATCATCCAA
970	980	990	1000	1010	1020
ACTCCCTATG	TGTCAATCAT	GATTTTAAAC	ACGTATGCCA	CCGTAGGATG	GCCGATGGAA
1030	1040	1050	1060	1070	1080
TGCGCCGATC	TAAC TAGACG	CCGAGTCATC	AACACGTTTT	CCCGTCTCGT	CCCCAATCTA
1090	1100	1110	1120	1130	1140
CATTCATGGG	TCAACCCCAT	CCTCTACGCT	CTCATGGGAA	ATGACTTTGT	GTCTAAAGTG
1150	1160	1170	1180	1190	1200
GGCCAATGCT	TTGGGGGGGA	ACTCACGAAC	CGTCGAACTT	TTCTGCGTTC	CAAGCAACAA
1210	1220	1230	1240	1250	1260
GCCCGCAACT	CGGACGATGT	ACCGACAATT	GTCAGTCAAC	AACCCGCCAC	ACCCACCATC

FIG. 7A

RhUL33 spliced

1270	1280	1290	1300	1310	1320
GTCAATAAGC	CCGAAAAAAA	CCCGCACGTA	AAACGCGGTG	TATCTTTCAG	CGTCAGCGCA
1330	1340	1350	1360	1370	1380
TCTTCCGAAC	TCGCAGCGGC	CAAAAAAGCC	AAAGACAAAG	CCAAGCGGCT	TTCCATGTCC
1390	1400	1410	1420	1430	1440
CACCAAAACC	TACGTCTGAC	GTGA.....

RhUL78

10	20	30	40	50	60
ATGATTACGG	AGCGCGTCCT	CGCAGGCATC	CTCGCGGGCA	TGACGGCCGC	GGGGAGTTTG
70	80	90	100	110	120
GTCATTCTCC	TCGCGGTTGT	TATGTGGTTG	AACATGTTAG	ATCGCGCTGG	CATGCCAATG
130	140	150	160	170	180
GCCGTTGGGC	ATTACACAGG	GAACCTGGTG	TTGACTCAGG	TCATCTGTAT	CTTCTCCATG
190	200	210	220	230	240
CTGGCGTCTA	AAATTGTTGG	CATGACGAGT	GCGGCCAACA	TGGGCTTCTG	CGGCATCGTG
250	260	270	280	290	300
GTTTTTCTGG	AAGACACTGG	CCTCTATGTC	ACCTCGCTGC	TCTTCATGTT	TATGATCCTG
310	320	330	340	350	360
GATCGCATGG	CGGCTTTTCT	TAACGGGCGT	CTTTTCTGGA	GGCAGCAGAC	GACGAAGCAG
370	380	390	400	410	420
AATCTGAGTA	CAAGCGTGTA	CATTATTCTG	TTTTGCTGGG	TGTTGGGAAT	GGCCGCGGCT
430	440	450	460	470	480
GTTCCAGCG	CGGCTGTGGC	TGCACCCAAT	TCCAGGTGGG	AACGCTGCCA	AATTCAGTG
490	500	510	520	530	540
TCATATGCCG	CAATCGACAT	GATTGTGAAG	CTCTGGTTTG	TGCTGTTGGC	ACCCGTCGTG
550	560	570	580	590	600
CTGATTATGG	CTGTGATCAT	TCAATCTTCC	TATCATCGTG	ATCGGGAGAG	GATCTGGTAC
610	620	630	640	650	660
TATGCCAGAC	GTGTGTTTAT	GTTCTACACG	GCCTGCTTTG	TCATGATGGT	GCCTTATTAC
670	680	690	700	710	720
TTGCTCAGAG	TCATGCTGAG	CGACTTTGCT	TTGGTTGATA	TAAAAACAAA	AACGGCGAAC
730	740	750	760	770	780
AGCGACGGTT	GTGATTCGAC	ATTTCTTGAT	TATCTGAACA	TGTTCACTCA	CGTGATTTAC
790	800	810	820	830	840
AGTTTTAAGT	TGGTGGTGTT	TGCTTTGTTT	ATTGTCCTGT	TTTGCTCCAT	AAACCCGATG
850	860	870	880	890	900
GAAACGCTGG	AAGAATGCTT	GGAGAGGGCC	GATGCTGAGA	GGCAAAGTCG	GTCAGAAGCA
910	920	930	940	950	960
TCCCAGGGTG	AAAGGAGGCT	GCCAATCAAC	ACATGCTGTA	TAAAGTTGAT	TGAATTGATA
970	980	990	1000	1010	1020
AAGCAGTATG	TAAGCACTCT	CTCTAAAGCC	ACGAGGGACA	ATTCTGGCGA	AAGGGCCAAT
1030	1040	1050	1060	1070	1080
TTGCCAGAGA	ATGCTGAAGA	TATTGGAACA	ACTGGCAGTG	ATCAGCTACC	GACTGAGGTC
1090	1100	1110	1120	1130	1140
ACCGTGACCC	CAAATTCATC	GGCTGTGTTT	AGCACTGGAG	GAACGGTGTC	TCCAGTCTAA
1150	1160	1170	1180	1190	1200
.....